

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/777,566

DATE: 04/25/2001

TIME: 18:21:25

Input Set : N:\Crf3\RULE60\09777566.txt

Output Set: N:\CRF3\04252001\I777566.raw

ENTERED

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4 <110> APPLICANT: Kretz, Keith
6 <120> TITLE OF INVENTION: NOVEL PHYTASE
9 <130> FILE REFERENCE: 09010/029003
11 <140> CURRENT APPLICATION NUMBER: 09/777,566
12 <141> CURRENT FILING DATE: 2001-02-05
14 <150> PRIOR APPLICATION NUMBER: 09/318,528
15 <151> PRIOR FILING DATE: 1999-05-25
17 <150> PRIOR APPLICATION NUMBER: 08/910,798
18 <151> PRIOR FILING DATE: 1997-08-13
20 <150> PRIOR APPLICATION NUMBER: 09/259,214
21 <151> PRIOR FILING DATE: 1999-03-01
23 <160> NUMBER OF SEQ ID NOS: 4
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 1323
29 <212> TYPE: DNA
30 <213> ORGANISM: Escherichia coli
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)...(1320)
36 <221> NAME/KEY: misc_feature
37 <222> LOCATION: (1)...(1323)
38 <223> OTHER INFORMATION: n = A,T,C or G
40 <400> SEQUENCE: 1
41 atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg tta acc      48
42 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
43 1 5 10 15
45 ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt      96
46 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
47 20 25 30
49 gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg      144
50 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
51 35 40 45
53 caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta      192
54 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
55 50 55 60
W--> 57 aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc tat ctc      240
58 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
59 65 70 75 80
61 gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg gcg aaa      288
62 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
63 85 90 95
65 aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat gtc gac      336
66 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
67 100 105 110
69 gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg gca cct      384
70 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro

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71          115          120          125
73 gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt ccc gat      432
74 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
75          130          135          140
77 ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat aac gcg      480
78 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
79 145          150          155          160
81 aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att gct gac      528
82 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
83          165          170          175
85 ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg gtg ctt      576
86 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
87          180          185          190
89 aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag gac gaa      624
90 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
91          195          200          205
93 agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg agc gcc      672
94 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
95          210          215          220
97 gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg ctg acg      720
98 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
99 225          230          235          240
101 gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg ggg tgg      768
102 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
103          245          250          255
105 gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat      816
106 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
107          260          265          270
109 aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc      864
110 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
111          275          280          285
113 cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat      912
114 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
115          290          295          300
117 cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg      960
118 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
119 305          310          315          320
121 ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg      1008
122 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
123          325          330          335
125 gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt      1056
126 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
127          340          345          350
129 ggt gaa ctg gtg ttt gaa cgc tgg cgt ccg cta agc gat aac agc cag      1104
130 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
131          355          360          365
133 tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat      1152
134 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
135          370          375          380

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```

137 aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc      1200
138 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
139 385                               390                               395                               400
141 ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca      1248
142 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
143                               405                               410                               415
145 ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg      1296
146 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
147                               420                               425                               430
149 aga tct cat cac cat cac cat cac taa                                1323
150 Arg Ser His His His His His His
151                               435                               440
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 440
156 <212> TYPE: PRT
157 <213> ORGANISM: Escherichia coli
159 <400> SEQUENCE: 2
160 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr
161 1                               5                               10                               15
162 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser
163                               20                               25                               30
164 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr
165                               35                               40                               45
166 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val
167 50                               55                               60
168 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu
169 65                               70                               75                               80
170 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys
171                               85                               90                               95
172 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp
173                               100                              105                              110
174 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro
175                               115                              120                              125
176 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp
177 130                              135                              140
178 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala
179 145                              150                              155                              160
180 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp
181                               165                               170                               175
182 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu
183                               180                               185                               190
184 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu
185                               195                               200                               205
186 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala
187 210                               215                               220
188 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr
189 225                               230                               235                               240
190 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp
191                               245                               250                               255

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192 Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His
193           260           265           270
194 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser
195           275           280           285
196 Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His
197           290           295           300
198 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu
199 305           310           315           320
200 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu
201           325           330           335
202 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly
203           340           345           350
204 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln
205           355           360           365
206 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp
207           370           375           380
208 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr
209 385           390           395           400
210 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala
211           405           410           415
212 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu
213           420           425           430
214 Arg Ser His His His His His
215           435           440
217 <210> SEQ ID NO: 3
218 <211> LENGTH: 49
219 <212> TYPE: DNA
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Oligonucleotide
225 <400> SEQUENCE: 3
226 gtttctgaat tcaaggagga atttaaataa aagcgatctt aatcccatt
228 <210> SEQ ID NO: 4
229 <211> LENGTH: 33
230 <212> TYPE: DNA
231 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: Oligonucleotide
236 <400> SEQUENCE: 4
237 gtttctggat ccttacaacac tgcacgccg tat

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VERIFICATION SUMMARY

DATE: 04/25/2001

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TIME: 18:21:26

Input Set : N:\Crf3\RULE60\09777566.txt

Output Set: N:\CRF3\04252001\I777566.raw

L:57 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1